

SEQUENCE LISTING

<110> Rothschild, Max
Ciobanu, Dan
Malek, Massoud
Plastow, Graham

<120> Novel PRKAG3 Alleles and Use of the Same as Genetic Markers for Reproductive and Meat Quality Traits

<130> P04668US3

<150> 60/231045

<151> 2000-09-08

<150> 60/260,239

<151> 2001-01-08

<150> 60/299,111

<151> 2001-06-18

<160> 17

<170> PatentIn version 3.0

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<211> 1873

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<220>

<221> CDS

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ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag	192
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Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	
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His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
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Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
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Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
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Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly	
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gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac	288
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Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly	
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Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg	
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Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	
145 150 155 160	
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His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
165 170 175	
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt	576
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
180 185 190	
gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag	624
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys	
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Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
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Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
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Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	
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Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly			
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FOOTED 22005560

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Leu	Gly	Trp	Asp	Asp	Glu	Leu	Gln	Lys	Pro	Gly	Ala	Gln	Val	Tyr	Met	145	150	155
His	Phe	Met	Gln	Glu	His	Thr	Cys	Tyr	Asp	Ala	Met	Ala	Thr	Ser	Ser	165	170	175
Lys	Leu	Val	Ile	Phe	Asp	Thr	Met	Leu	Glu	Ile	Lys	Lys	Ala	Phe	Phe	180	185	190
Ala	Leu	Val	Ala	Asn	Gly	Val	Arg	Ala	Ala	Pro	Leu	Trp	Asp	Ser	Lys	195	200	205
Lys	Gln	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Leu	Val	210	215	220
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Glu	His	Lys	Ile	Glu	Thr	Trp	Arg	Glu	Ile	Tyr	Leu	Gln	Gly	Cys	Phe	245	250	255
Lys	Pro	Leu	Val	Ser	Ile	Ser	Pro	Asn	Asp	Ser	Leu	Phe	Glu	Ala	Val	260	265	270
Tyr	Ala	Leu	Ile	Lys	Asn	Arg	Ile	His	Arg	Leu	Pro	Val	Leu	Asp	Pro	275	280	285
Val	Ser	Gly	Ala	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys	290	295	300
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Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val	325	330	335
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Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
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Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
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Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
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Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly	
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Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	
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His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
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Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
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gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag	624
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Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
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Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr	

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305	310	315	320	
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg				1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val				
325		330	335	
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac				1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp				
340		345	350	
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg				1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val				
355		360	365	
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca				1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr				
370		375	380	
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca				1200
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr				
385		390	395	400
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg				1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly				
405		410	415	
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc				1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu				
420		425	430	
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc				1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile				
435		440	445	
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc				1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala				
450		455	460	
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga				1452
gccgtggact cagctctcac ttccctcag ccccaacttgc tgggtctggct cttgttcagg				1512
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atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagccttgt				1632
gaaatctacc agcatcaaga ctactgtgg gaccactgct ttgtcccatt ctcagctgaa				1692
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtga				1752
gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt ccccccctgct				1812
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g				1873

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<212> PRT
<213> Sus scrofa

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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45

Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

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"00160"22005560

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala

460

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Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe

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gcc ctg gtg gcc aac ggc atc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205			624
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220			672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240			720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255			768
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260 265 270			816
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275 280 285			864
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys 290 295 300			912
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr 305 310 315 320			960
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val 325 330 335			1008
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp 340 345 350			1056
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val 355 360 365			1104
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr 370 375 380			1152
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr 385 390 395 400			1200
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly 405 410 415			1248
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc			1296

Glu Val Ile Asp Arg Ile Val Arg	Glu Gln Val His Arg Leu Val Leu	
420	425	430
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc		1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile		
435	440	445
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc		1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala		
450	455	460
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga		1452
gccgtggact cagctctcac ttccctcag cccacttgc tggctctggct cttgttcagg		1512
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gaaatctacc agcatcaaga ctactgtgg gaccactgct ttgtccatt ctcagctgaa		1692
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gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt cccccctgct		1812
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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala		
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly		
35	40	45
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln		
50	55	60
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu		
65	70	75 80
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp		
85	90	95

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325

330

335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
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<212> DNA
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<220>
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gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30
tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45
ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln

60

gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu 65 70 75 80	240
gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp 85 90 95	288
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly 100 105 110	336
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val 115 120 125	384
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg 130 135 140	432
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met 145 150 155 160	480
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser 165 170 175	528
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe 180 185 190	576
gcc ctg gtg gcc aac ggc gtc caa gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205	624
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220	672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240	720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa gcc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255	768
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260 265 270	816
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275 280 285	864
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag ccg ctt ctc aag	912

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Phe	Leu	His	Ile	Phe	Gly	Thr	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr	
305					310					315					320	
cgc	acc	atc	caa	gat	ttg	ggc	atc	ggc	aca	ttc	cga	gac	ttg	gcc	gtg	1008
Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val	
				325					330						335	
gtg	ctg	gaa	acg	gcg	ccc	atc	ctg	acc	gca	ctg	gac	atc	ttc	gtg	gac	1056
Val	Leu	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp	
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Arg	Arg	Val	Ser	Ala	Leu	Pro	Val	Val	Asn	Glu	Thr	Gly	Gln	Val	Val	
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ggc	ctc	tac	tct	cgc	ttt	gat	gtg	atc	cac	ctg	gct	gcc	caa	caa	aca	1152
Gly	Leu	Tyr	Ser	Arg	Phe	Asp	Val	Ile	His	Leu	Ala	Ala	Gln	Gln	Thr	
						375									380	
tac	aac	cac	ctg	gac	atg	aat	gtg	gga	gaa	gcc	ctg	agg	cag	cgg	aca	1200
Tyr	Asn	His	Leu	Asp	Met	Asn	Val	Gly	Glu	Ala	Leu	Arg	Gln	Arg	Thr	
						390					395				400	
ctg	tgt	ctg	gaa	ggc	gtc	ctt	tcc	tgc	cag	ccc	cac	gag	acc	ttg	ggg	1248
Leu	Cys	Leu	Glu	Gly	Val	Leu	Ser	Cys	Gln	Pro	His	Glu	Thr	Leu	Gly	
				405						410					415	
gaa	gtc	att	gac	cgg	att	gtc	cgg	gaa	cag	gtg	cac	cgc	ctg	gtg	ctc	1296
Glu	Val	Ile	Asp	Arg	Ile	Val	Arg	Glu	Gln	Val	His	Arg	Leu	Val	Leu	
				420						425					430	
gtg	gat	gag	acc	cag	cac	ctt	ctg	ggc	gtg	gtg	tcc	ctc	tct	gac	atc	1344
Val	Asp	Glu	Thr	Gln	His	Leu	Leu	Gly	Val	Val	Ser	Leu	Ser	Asp	Ile	
				435						440					445	
ctt	cag	gct	ctg	gtg	ctc	agc	cct	gct	gga	att	gat	gcc	ctc	ggg	gcc	1392
Leu	Gln	Ala	Leu	Val	Leu	Ser	Pro	Ala	Gly	Ile	Asp	Ala	Leu	Gly	Ala	
				450						455					460	
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<400> 10

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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
 35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
 50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
 65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
 85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
 100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
 115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
 130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
 145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
 165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
 180 185 190

Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys

195

200

205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
 435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
 450 455 460

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 <213> Sus scrofa

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 tcttcaggac cccaatctcc cccactccac tcgcctggct cttgtcttcc tctcctttgc 180
 cttctttgtt ccgctttgtt tcttcttctc cctctcctc cactctctcc ctctttcaaa 240
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